GNPAnnot
Community Annotation System (CAS)

Système d'annotation communautaire de génomes de plantes, d'insectes et de champignons

GTGC workshop Sep 10th, 2010

S. BOCS

Project

- Granted by the French National Research Agency

- A community system of structural and functional annotation supported by comparative genomics and dedicated to plant, insect and fungus genomes allowing both automatic predictions and manual curations of genomic objects.

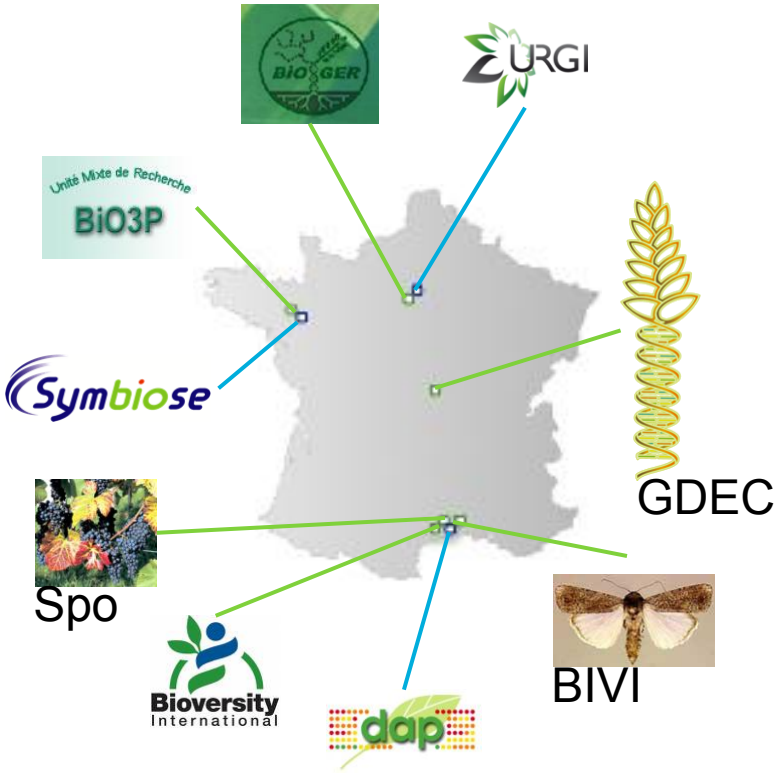
- 5 work packages
  - database and flow management
  - annotator interfaces implementation
  - interoperability with other systems
  - sequence exploitation and platform release
  - manual annotation and CAS validation

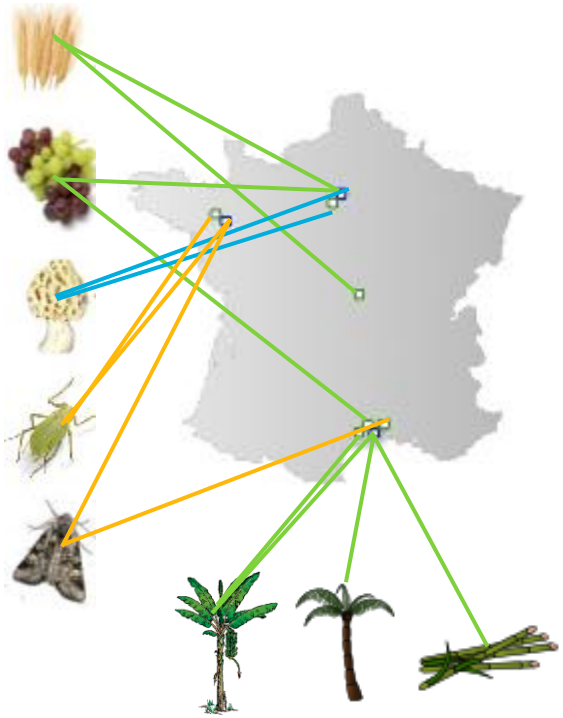
Resources

9 Partners

3 Bioinformatics platforms

>8 Studied species





http://www.gnpannot.org/

GNPAnnot Portal

QuickR

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Search this site:

Search

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  - Monocots e-Learning Courses
  - Monocots Tutorials
  - Chado Controller
  - Publications
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- Contact

Languages

- English
- Français

About GNPAnnot

GNPAnnot is a project on green genomics which intends to develop a community system of structural and functional annotation supported by comparative genomics and dedicated to plant, insect and fungus genomes allowing both automatic predictions and manual curations of genomic objects.

Read more

Community Annotation Systems

Musa

Arecaceae

SpodoBase

Coffee

Cocoa

AphidBase

Sugarcane

TriAnnot Pipeline

Vitis

Fungal Platform

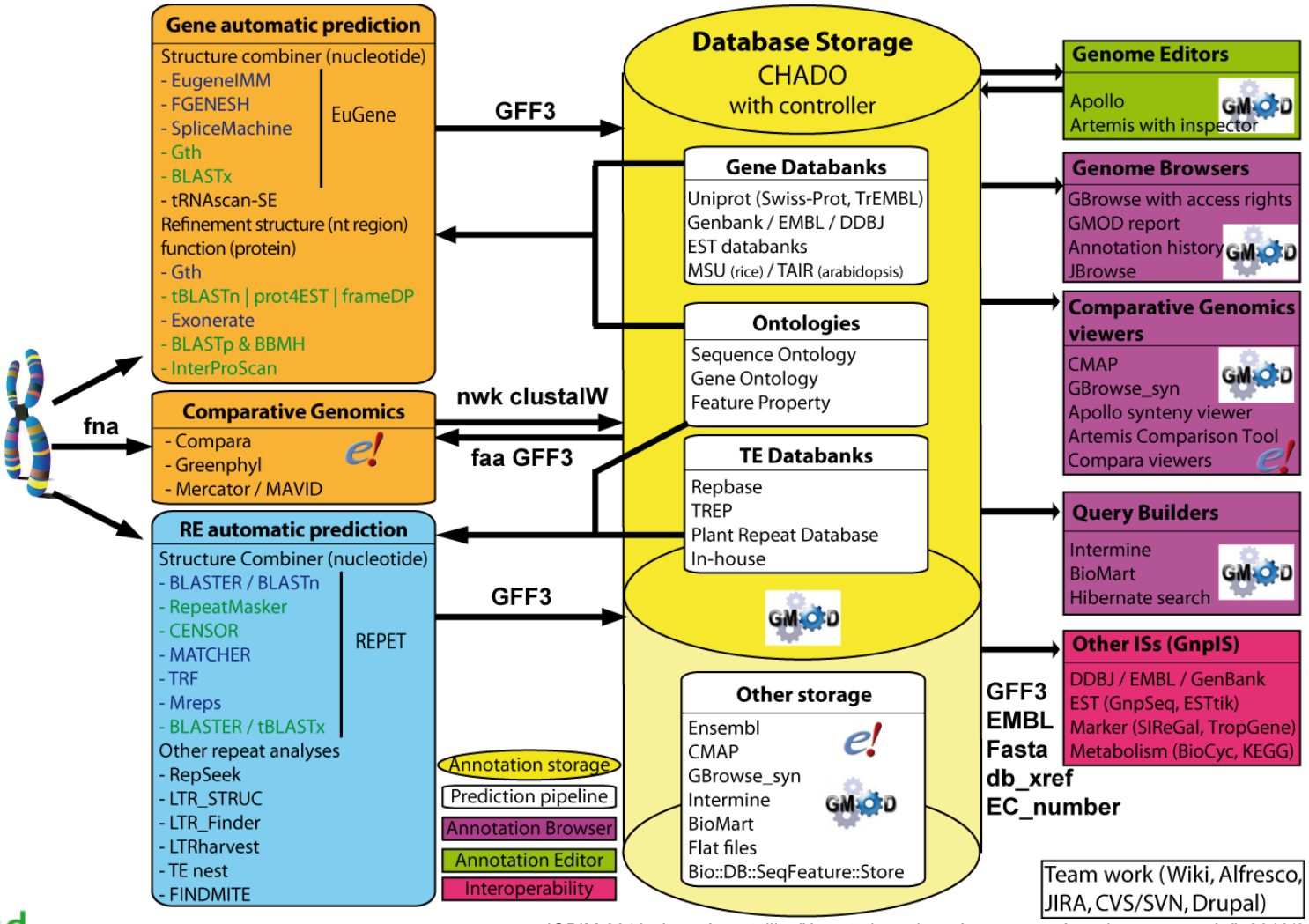
GNPAnnot Partners

UMR DAP, URGI, UMR BIOGER, UMR BIO3P, UMR BIVI, Bioversity, UMR GDEC, UMR SPO

Read more

Architecture Concept

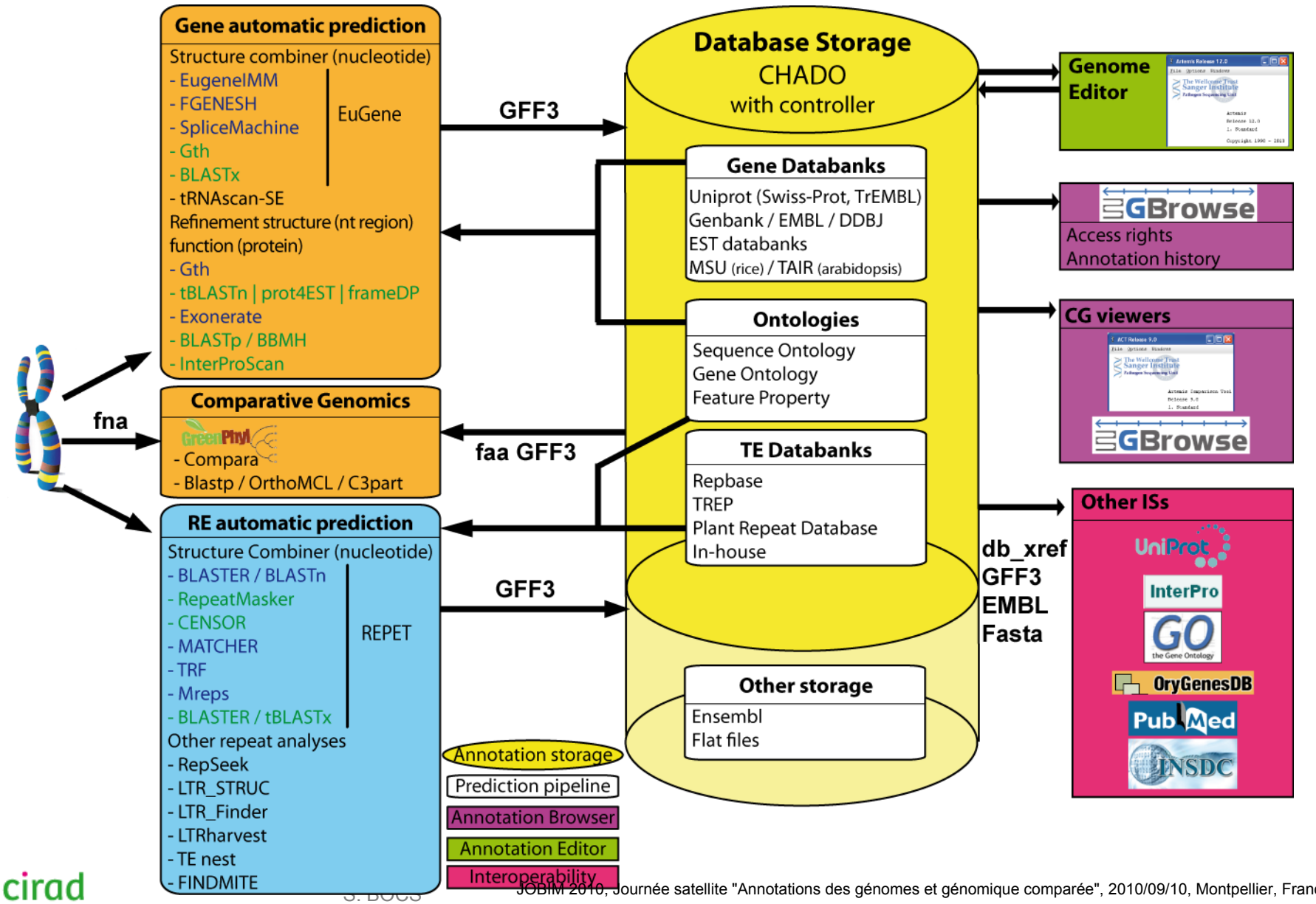
The Community Annotation System (CAS) is user-friendly, generic, modular, portable, sustainable, upgradable and compatible



Focus

- 3 applications of CAS to show genericity & modularity of the architecture
  - Tropical plant CAS (Montpellier)
  - Insect CAS (Rennes)
  - Fungal CAS (Versailles)
- Innovation
  - Chado Controller
  - Genome report system
- Comparative Genomics
  - Ensembl Compara
  - In-house syntenic regions
  - PhylomeDB
  - Gbrowse_syn

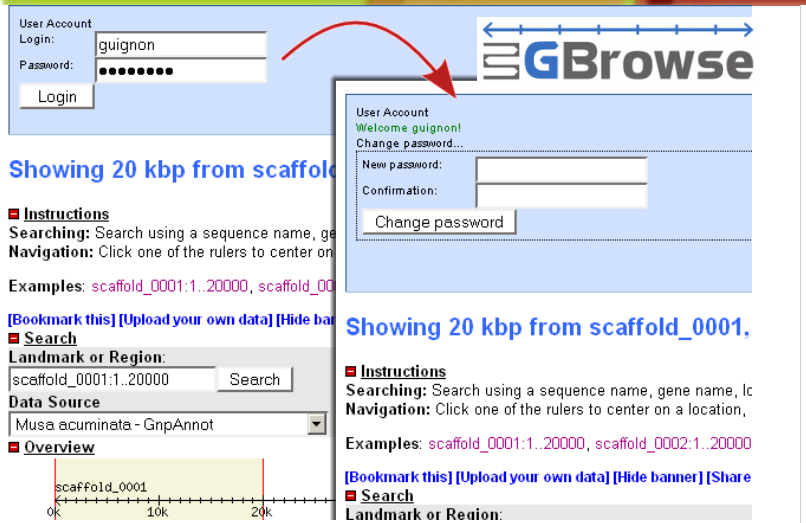
Tropical Plant CAS



Tropical Plant CAS
Chado Controller

- Chado Controller: un superviseur pour la confidentialité, la qualité et le suivi des annotations [JOBIM 2010 poster 68]
  - Feature confidentiality → Access Restriction
  - Manual annotation quality → Annotation Inspector
  - Manual annotation tracking → Annotation History

Tropical Plant CAS Access Restriction



Musa acuminata - GnpAnnot . Contigs . Management

User Account
Change password...

Logout gnpannot_admin

Database: gnpannot_musa
Authentication module: Bio::Graphics::Browser::AuthExtDB
Authentication database: gnpannot_accounts

Edit Feature Access

Feature: **scaffold_0001** (Ma4001J14, MA4-1J14)

Group Name	Change Access				
	Keep current	Use default	Forbiden	Read	Write
BSV	○	◉	○	○	○
RGA	○	◉	○	○	○
anonymous	○	○	○	◉	○
public_annotator	○	○	○	○	◉

Annotator Name	Groups	Change Access				
		Keep current	Use default	Forbiden	Read	Write
chabannes	public_annotator, BSV	○	◉	○	○	○
droc	RGA, public_annotator, BSV	○	◉	○	○	○
fcbaurens	RGA, public_annotator, BSV	○	◉	○	○	○
gnpannot_admin	RGA, public_annotator, BSV	○	○	○	○	◉
gnpannot_gbrowse		○	◉	○	○	○
guest	public_annotator	○	○	○	◉	○
guignon	RGA, public_annotator, BSV	○	◉	○	○	○

Musa acuminata - GnpAnnot Annotators Manageme

User Account
Change password...

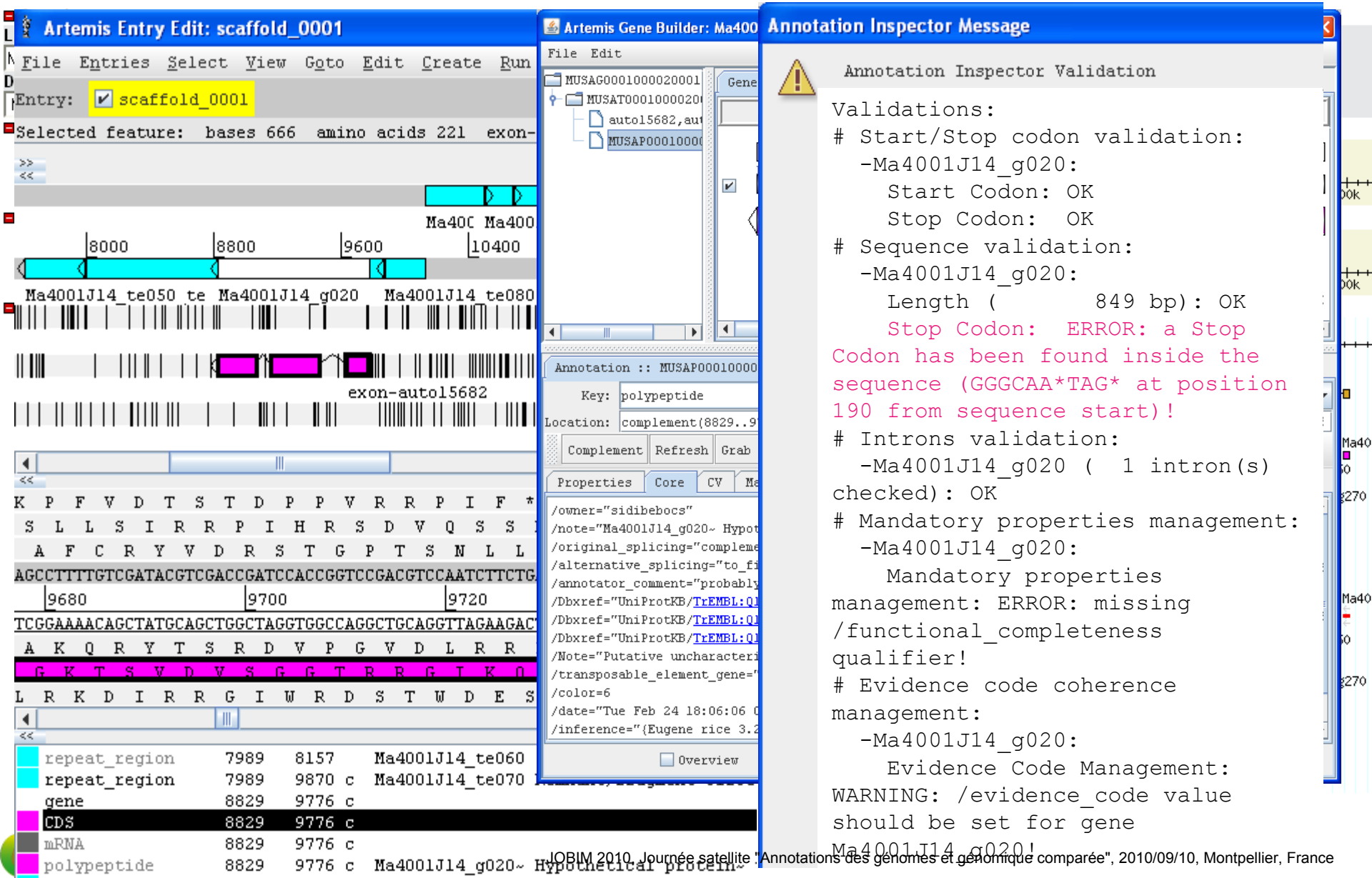
Database: gnpannot_musa
Authentication module: Bio::Graphics::Browser::AuthExtDB
Authentication database: gnpannot_accounts

Users Menu

- Create a new user
- << Back to Main Menu

ID	User Name	Groups	Flags								Role	Comments	
			Disabled	Locked	No Password	Password Locked	Password to Change	Write Access	Gene Editor Access	Admin			
16	wanghao	public_annotator	-	-	-	-	√	-	-	-			Edit Remove
8	droc	RGA, public_annotator, BSV	-	-	-	-	-	√	√	√	CIRAD	Gaetan Droc	Edit Remove
20	urgi		-	-	-	√	-	-	√	-	URGI	Compte pour acces en lecture seule a tout.	Edit Remove
11	chabannes	public_annotator, BSV	-	-	-	-	-	√	√	-		Matthieu Chabannes	Edit Remove
13	bennetzen	public_annotator	-	-	-	-	√	√	√	-		Jeff Bennetzen	Edit Remove

Tropical Plant CAS Annotation Inspector



Tropical Plant CAS Annotation History

GMGC home page | Clone search | Genome browser | Blast

Search

Date: 23:06 02/09/2010
Author: sidibebocs

Gene: Complement(8829..9776)
mRNA: Complement(8829..9776)
Exon: [+]**Complement(Join(8829..9059, 9159..9776))** - 23:06 02/09/2010
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/note="**Ma4001J14_g020~ Hypothetical protein~ unknown_gene~ missing_completeness**"
/annotator_comment="probably artefact or TE protein"
/inference="{Eugene rice 3.2}"
Product="Hypothetical protein"
Evidence Code="ISS"
EC_number="unknown_EC_number"
/locus_tag="Ma4001J14_g020"

Date: 11:19 11/06/2010
Author: gnpannot_admin

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mRNA: Complement(8829..9776)
Exon: Complement(Join(8829..9059, 9159..9459, 9643..9776))
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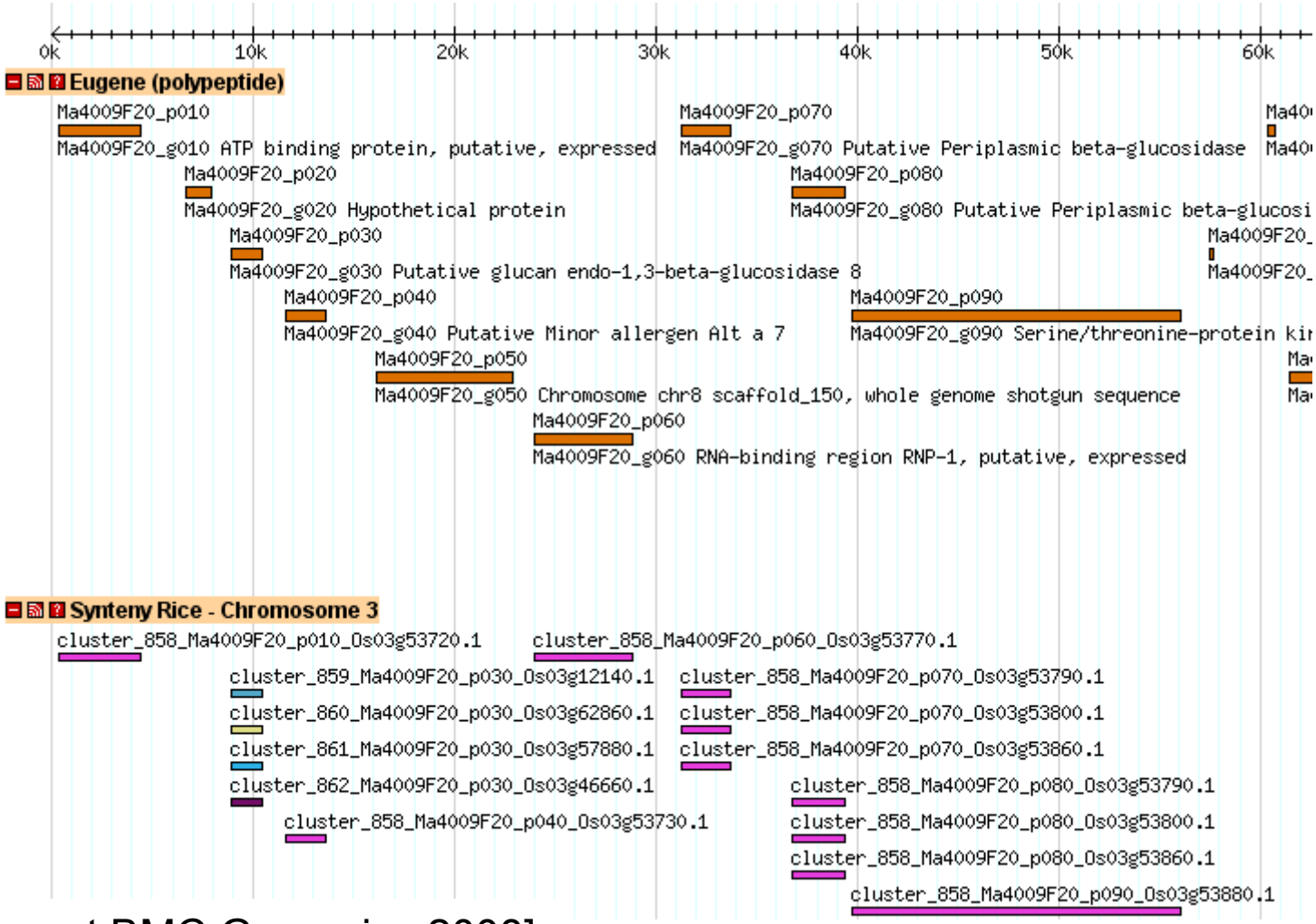
/note="Ma4001J14_g020 Hypothetical protein"
/annotator_comment="probably artefact or TE protein"
/inference="{Eugene rice 3.2}"
Product="Hypothetical protein"
Evidence Code="**ISS**"
EC_number="**unknown_EC_number**"
/locus_tag="Ma4001J14_g020"

Tropical Plant CAS Microsynteny

Blastp, OrthoMCL, C3part between Musa proteomes per BAC & Oryza sativa proteomes per chromosomes



[Lescot BMC Genomics 2008]

Tropical Plant CAS Microsynteny

Showing 79.63 kbp from Ma4052E23, positions 1 to 79,629

[BOCS BMC Plant Bio 2010]

Instructions
Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed.
Navigation: Click one of the rulers to center on a location, or click and drag to select a region. Use the Scroll/Zoom buttons to change magnification and position.

Examples: scaffold_0001:1..20000, scaffold_0002:1..20000, scaffold_0003:1..20000, scaffold_0004:1..20000, Ma4002G17, MaC139M12.

[Bookmark this] [Upload your own data] [Hide banner] [Share these tracks] [Link to Image] [High-res Image] [Help] [Reset]

Search

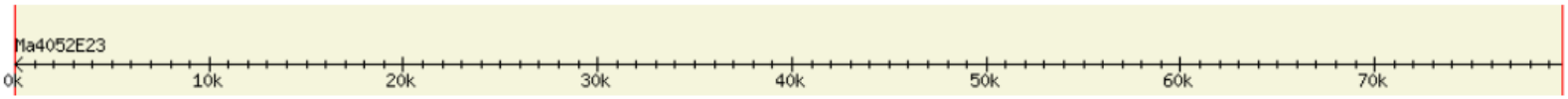
Landmark or Region: Ma4052E23 Search

Data Source: Musa acuminata - GnpAnnot

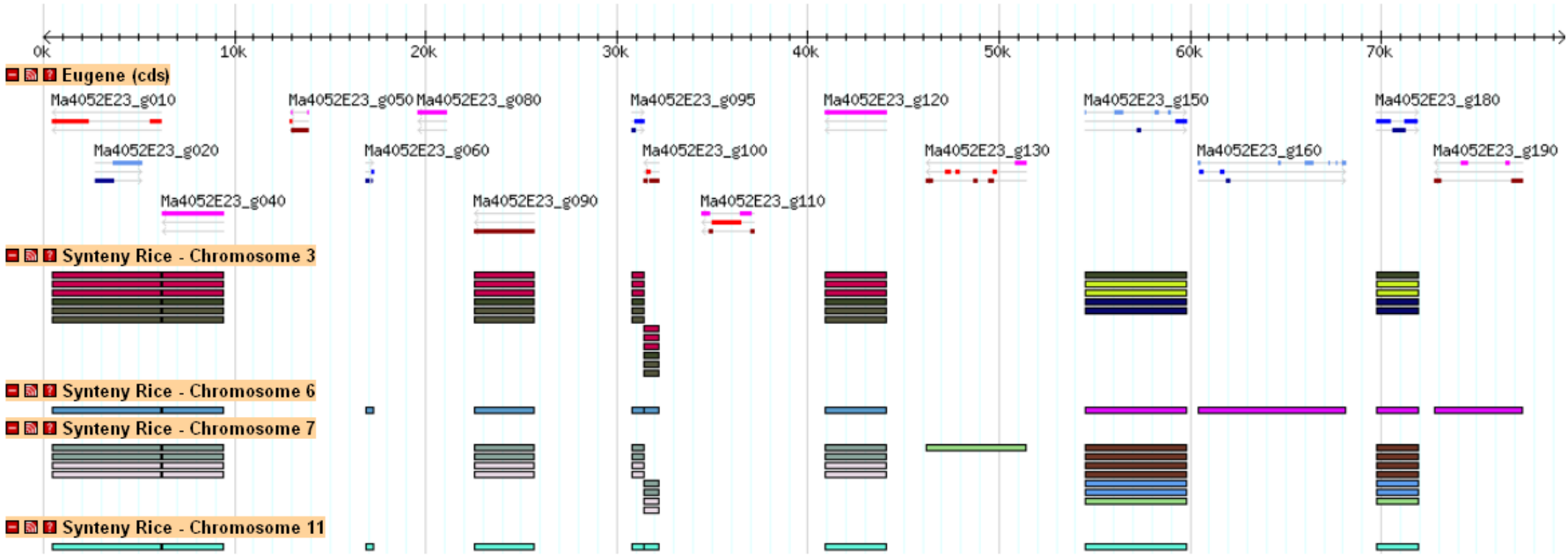
Reports & Analysis: Annotate Restriction Sites Configure... Go

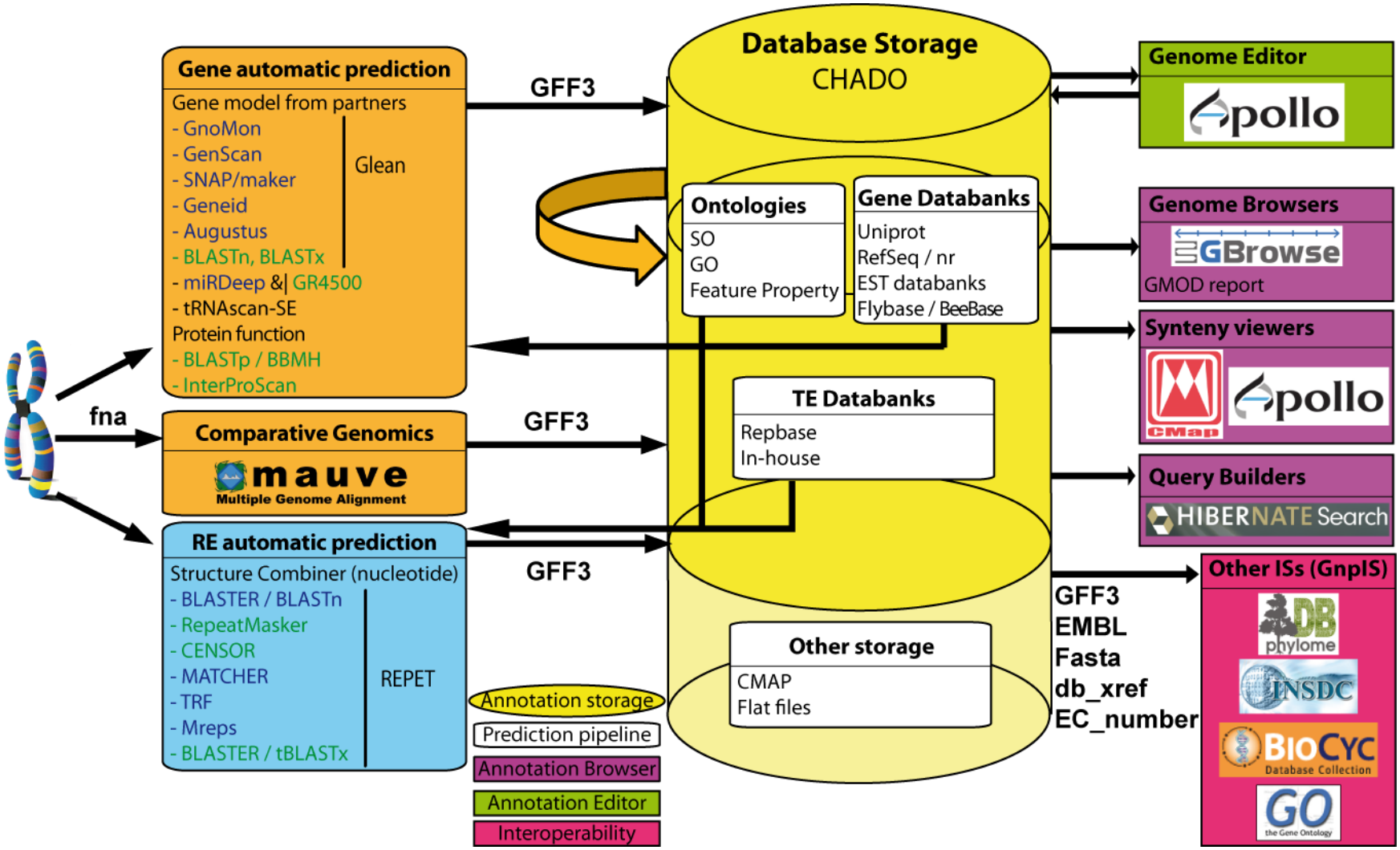
Scroll/Zoom: Show 79.63 kbp **Flip**

Overview

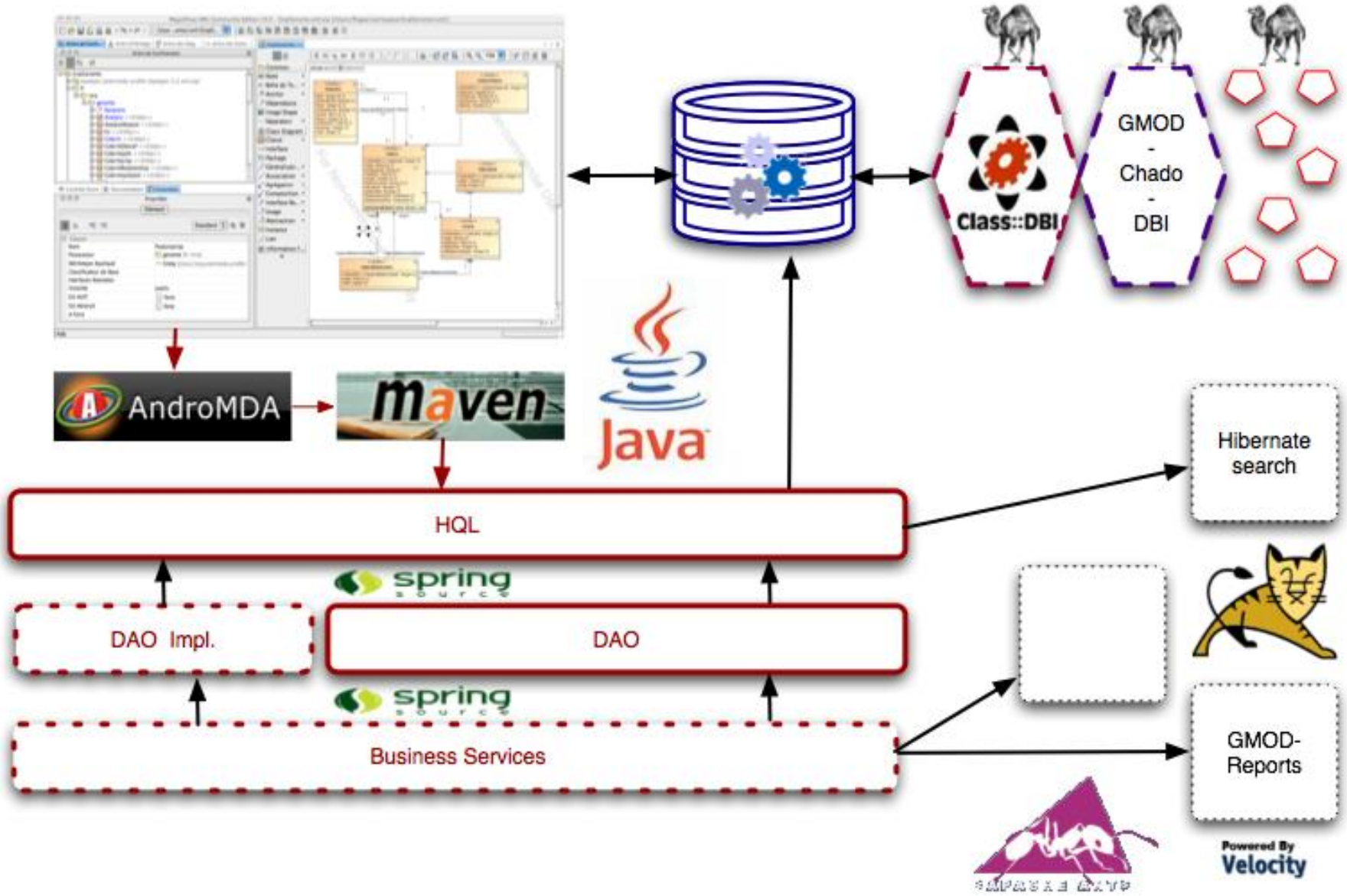


Details



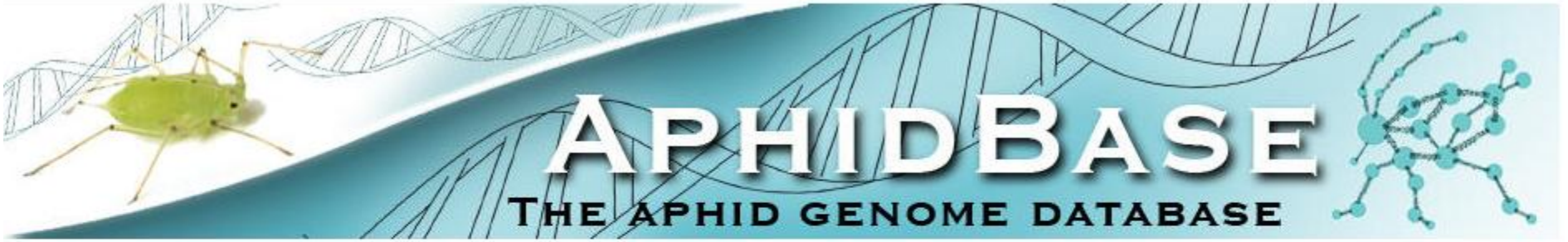

Gene automatic prediction
Gene model from partners
- GnoMon
- GenScan
- SNAP/maker
- Geneid
- Augustus
- BLASTn, BLASTx
- miRDeep & GR4500
- tRNAscan-SE
Glean
Protein function
- BLASTp / BBMH
- InterProScan
GFF3
Database Storage
CHADO
Genome Editor
Apollo
Ontologies
SO
GO
Feature Property
Gene Databanks
Uniprot
RefSeq / nr
EST databanks
Flybase / BeeBase
Genome Browsers
GBrowse
GMOD report
Synteny viewers
CMap
Apollo
fna
Comparative Genomics
mauve
Multiple Genome Alignment
GFF3
TE Databanks
Repbase
In-house
Query Builders
HIBERNATE Search
RE automatic prediction
Structure Combiner (nucleotide)
- BLASTER / BLASTn
- RepeatMasker
- CENSOR
- MATCHER
- TRF
- Mreps
- BLASTER / tBLASTx
REPET
GFF3
Other storage
CMAP
Flat files
GFF3
EMBL
Fasta
db_xref
EC_number
Other ISs (GnpIS)
DB phylome
INSDC
BioCyc Database Collection
GO the Gene Ontology
Annotation storage
Prediction pipeline
Annotation Browser
Annotation Editor
Interoperability

Genome report system



Search

Home page | Genomic Resources | Tools | Downloads | Links



Home page

*

Gbrowse | Apollo | Blast | PhylomeDB | AcypiCyc | GO

Quick Search

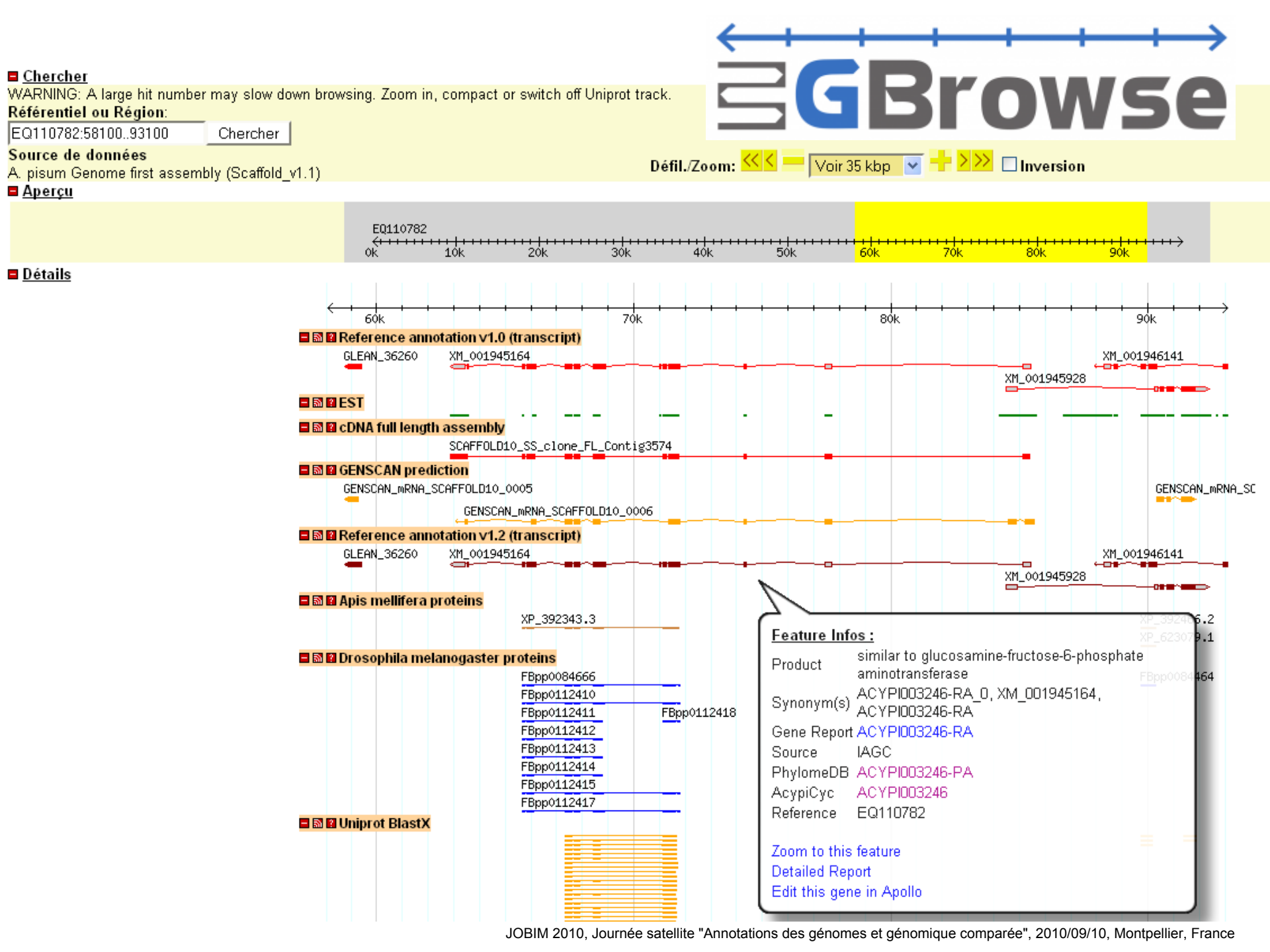
Envoyer

News

- **Plos Biology Genome article**
- GENOME Publications
- IAGC BOARD
- XXIV International Congress of Entomology, Korea, 2012
- 5th Phylloxera International Symposium
- Go to IAGC Membership page

Community Links

- Aphid Species File
- International Aphid Genomic Consortium
- Aphid genomic list server
- WiKi
- The Pea aphid


GBrowse
Chercher
WARNING: A large hit number may slow down browsing. Zoom in, compact or switch off Uniprot track.
Référentiel ou Région:
EQ110782:58100..93100
Chercher
Source de données
A. pisum Genome first assembly (Scaffold_v1.1)
Défil./Zoom:
Voir 35 kbp
Inversion
Aperçu
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40k
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Détails
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70k
80k
90k
Reference annotation v1.0 (transcript)
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XM_001945928
EST
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GENSCAN_mRNA_SC
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Drosophila melanogaster proteins
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FBpp0112418
FBpp0112412
FBpp0112413
FBpp0112414
FBpp0112415
FBpp0112417
Uniprot BlastX
Feature Infos :
Product
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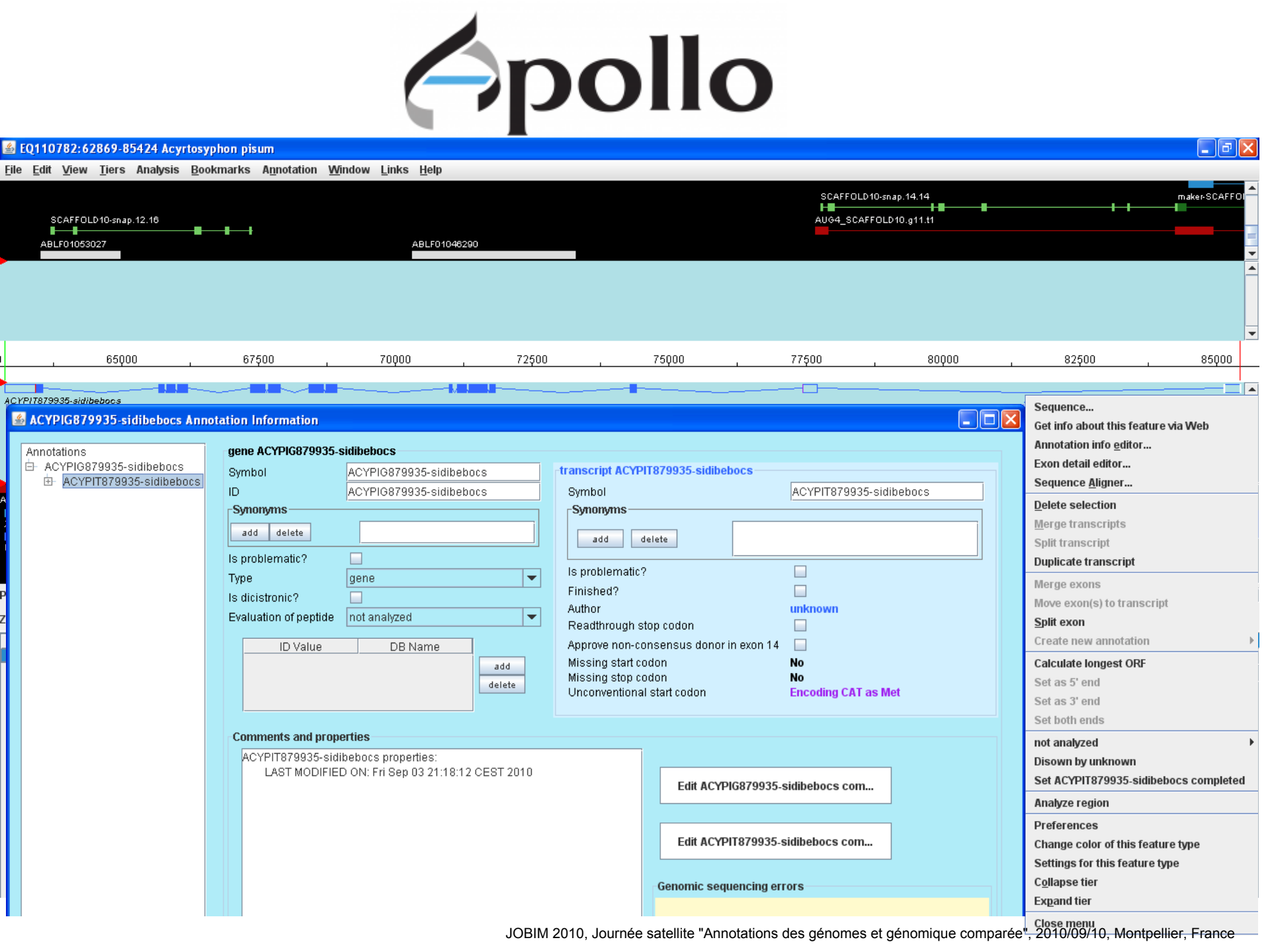
Synonym(s)
ACYPI003246-RA_0, XM_001945164, ACYPI003246-RA
Gene Report
ACYPI003246-RA
Source
IAGC
PhylomeDB
ACYPI003246-PA
AcypiCyc
ACYPI003246
Reference
EQ110782
Zoom to this feature
Detailed Report
Edit this gene in Apollo


Apollo
EQ110782:62869-85424 Acyrtosyphon pisum
File Edit View Tiers Analysis Bookmarks Annotation Window Links Help
SCAFFOLD10-snap.12.16
ABLF01053027
ABLF01046290
SCAFFOLD10-snap.14.14
AUG4_SCAFFOLD10.g11.t1
65000 67500 70000 72500 75000 77500 80000 82500 85000
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Symbol ACYPIG879935-sidibebocs
ID ACYPIG879935-sidibebocs
Synonyms
add delete
Is problematic?
Type gene
Is dicistronic?
Evaluation of peptide not analyzed
ID Value DB Name
add delete
transcript ACYPIT879935-sidibebocs
Symbol ACYPIT879935-sidibebocs
Synonyms
add delete
Is problematic?
Finished?
Author unknown
Readthrough stop codon
Approve non-consensus donor in exon 14
Missing start codon No
Missing stop codon No
Unconventional start codon Encoding CAT as Met
Comments and properties
ACYPIT879935-sidibebocs properties:
LAST MODIFIED ON: Fri Sep 03 21:18:12 CEST 2010
Edit ACYPIG879935-sidibebocs com...
Edit ACYPIT879935-sidibebocs com...
Genomic sequencing errors
Sequence...
Get info about this feature via Web
Annotation info editor...
Exon detail editor...
Sequence Aligner...
Delete selection
Merge transcripts
Split transcript
Duplicate transcript
Merge exons
Move exon(s) to transcript
Split exon
Create new annotation
Calculate longest ORF
Set as 5' end
Set as 3' end
Set both ends
not analyzed
Disown by unknown
Set ACYPIT879935-sidibebocs completed
Analyze region
Preferences
Change color of this feature type
Settings for this feature type
Collapse tier
Expand tier
Close menu

APHIDBASE
THE APHID GENOME DATABASE

Transcript Report

ACYPI003246-RA

Description

ID	XM_001945164
Name	XM_001945164
Synonym	ACYPI003246-RA_0
Synonym	ACYPI003246-RA
Synonym	XM_001945164

Genomic Position

Gbrowse

Sequence

Protein

Similarity

OtherProperties

product	similar to glucosamine-fructose-6-phosphate aminotransferase
curation_status	unchecked

Similarity

Transcript alignments

organism	tissue_type	clone_lib	Start	End	Strand	Name
Acyrthosiphon pisum	Whole body, nymphs and adults, winged and wingless	Pea aphid whole body normalized full length cDNA library	62873	63544	+	EX620011
Acyrthosiphon pisum	Whole body, nymphs and adults, winged and wingless	Pea aphid whole body normalized full length cDNA library	62875	63442	+	EX644687
Acyrthosiphon pisum	Whole body, nymphs and adults, winged and wingless	Pea aphid whole body normalized full length cDNA library	62877	65713	+	EX637331
Acyrthosiphon pisum	Whole body, nymphs and adults, winged and wingless	Pea aphid whole body normalized full length cDNA library	63178	63551	+	FF329516
Acyrthosiphon pisum	Whole body, nymphs	NA library	66073	68651	-	EX618758
Acyrthosiphon pisum	Whole body, nymphs	NA library	70992	77486	-	EX654319
Acyrthosiphon pisum	Whole body, nymphs	NA library	71133	77472	-	EX643474
Acyrthosiphon pisum	Whole body, nymphs	NA library	71332	71659	+	FF328130
Acyrthosiphon pisum	Whole body, nymphs	NA library	71563	85383	-	EX636229
Acyrthosiphon pisum			62869	63368	-	CV848013
Acyrthosiphon pisum			62873	63522	-	DY223703
Acyrthosiphon pisum			63326	63551	-	CV845728
Acyrthosiphon pisum			62911	63551	-	DY230031
Acyrthosiphon pisum			63160	63530	-	CV828813
Acyrthosiphon pisum			63160	63530	-	CV830359
Acyrthosiphon pisum			63160	63530	-	CV834717
Acyrthosiphon pisum			63160	63530	-	CV837389
Acyrthosiphon pisum			63160	63530	-	CV839111
Acyrthosiphon pisum			63160	63551	-	CV831354
Acyrthosiphon pisum			68420	68672	-	CV831097
Acyrthosiphon pisum	whole bod		62869	63551	+	CN583870
Acyrthosiphon pisum	whole bod		67340	67595	-	CN582688
Acyrthosiphon pisum	whole bod		71332	71659	-	CN586139
Acyrthosiphon pisum	whole body, nymphs and adults	Acyrthosiphon pisum, Pea Aphid	77440	77685	-	CF587977
Acyrthosiphon pisum	whole body, nymphs and adults	Acyrthosiphon pisum, Pea Aphid	84236	84869	+	CF587560
Acyrthosiphon pisum	whole insect	ApMS	63160	63551	-	CN762688
Acyrthosiphon pisum	whole insect	ApMS	63160	63551	-	CN762896
Acyrthosiphon pisum	whole insect	ApMS	67340	67889	-	CN763553
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Acyrthosiphon pisum	whole insect	ApMS	77440	85424	-	CN756870

Summary of organism

value	Number	frequency
Acyrthosiphon pisum	32	1.0

Summary of tissue_type

value	Number	frequency
antennae	3	0.09375
whole insect	7	0.21875
Whole body, nymphs and adults, winged and wingless	9	0.28125
head	8	0.25
whole body, nymphs and adults	5	0.15625

Summary of clone_lib

value	Number	frequency
Pea aphid whole body normalized full length cDNA library	9	0.28125
ID0AEE	3	0.09375
ApHL3SD	1	0.03125
Acyrthosiphon pisum, Pea Aphid	5	0.15625
ApMS	7	0.21875
ID0ACC	7	0.21875

Protein Report

ACYPI003246-PA_1.0

+Description

+Gbrowse

+Sequence

+Transcript

-Similarity

Protein Similarities

query_name	analysis	hit_name	description	interpro_id	go	positions
XP_001945199	Coil	coil	coiled-coil	-	-	51-80
XP_001945199	Gene3D	G3DSA:3.40.50.10490	no description	-	-	324-544
XP_001945199	Gene3D	G3DSA:3.60.20.10	no description	-	-	1-321
XP_001945199	HMMPanther	PTHR10937	GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE	-	-	1-677
XP_001945199	HMMPfam	PF00310	GATase_2	IPR000583	Biological Process: metabolic process (GO:0008152)	1-207
XP_001945199	HMMPfam	PF01380	SIS	IPR001347	Molecular Function: sugar binding (GO:0005529), Biological Process: carbohydrate metabolic process (GO:0005975)	372-502,543-660
XP_001945199	HMMTigr	TIGR01135	glmS: glutamine-fructose-6-phosphate transam	IPR005855	Molecular Function: glutamine-fructose-6-phosphate transaminase (isomerizing) activity (GO:0004360), Cellular Component: cytoplasm (GO:0005737), Biological Process: carbohydrate biosynthetic process (GO:0016051)	1-677
XP_001945199	ProfileScan	PS51278	GATASE_TYPE_2	IPR017932	-	1-298
XP_001945199	superfamily	SSF53697	SIS domain	-	-	326-677
XP_001945199	superfamily	SSF56235	N-terminal nucleophile aminohydrolases (Ntn hydrolases)	-	-	1-304

+Proteome

+Classification

GRS - Gmod Report System - Chado Term Root Report - Mozilla Firefox

Fichier Édition Affichage Historique Marque-pages Outils ?

http://isyip.genouest.org:8080/grs-1.8/grs?objectID=GO:0004360&reportID=aphidbase_term_report

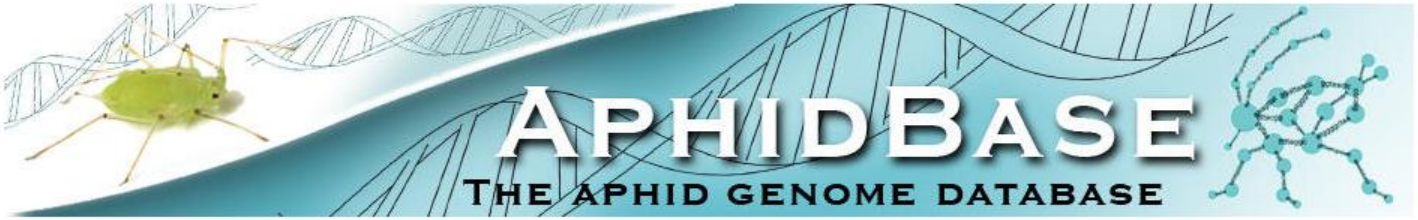
aphidbase

Musa acumi... | Musa acumi... | Musa acumi... | AphidBase: ... | GRS - ... | GRS - Gmod... | GRS - Gmod... | A. pisum Ge... | GRS - Gmod... | GRS - Gmod... | GRS - Gmod... | GRS - Gmod... | GRS - G

INRA

Bio-informatique Genouest

Homepage | GBrowse | Apollo | Genomic resources | Tools | Downloads | Links



Chado Term Hierarchy Report

TreeView

GO:0004360 : glutamine-fructose-6-phosphate transaminase (isomerizing) activity [1 product]

GO:0004360 : glutamine-fructose-6-phosphate transaminase (isomerizing) activity [1 product] Close

Show all occurrences of GO:0004360 in the classification

Accession	GO:0004360
Name	glutamine-fructose-6-phosphate transaminase (isomerizing) activity
Ontology	molecular_function
Definition	Catalysis of the reaction: L-glutamine + D-fructose 6-phosphate = L-glutamate + D-glucosamine 6-phosphate.
Synonyms	exact : D-fructose-6-phosphate amidotransferase activity exact : GlcN6P synthase activity exact : glucosamine 6-phosphate synthase activity exact : glucosamine--fructose-6-phosphate aminotransferase (isomerizing) activity exact : glucosamine-6-phosphate isomerase (glutamine-forming) activity exact : glucosamine-6-phosphate synthase activity exact : hexosephosphate aminotransferase activity exact : L-glutamine-D-fructose-6-phosphate amidotransferase activity exact : L-glutamine:D-fructose-6-phosphate isomerase (deaminating) broad : glucosaminephosphate isomerase
Cross-refs.	EC:2.6.1.16 MetaCyc:L-GLN-FRUCT-6-P-AMINOTRANS-RXN
Comment	none

Rechercher : 00436 Suivant Précédent Surligner tout Respecter la casse

Chado Term Report

GO:0004360

Description

Accession	GO:0004360
Name	glutamine-fructose-6-phosphate transaminase (isomerizing) activity
Ontology	molecular_function
Definition	Catalysis of the reaction: L-glutamine + D-fructose 6-phosphate = L-glutamate + D-glucosamine 6-phosphate.
Synonyms	exact : D-fructose-6-phosphate amidotransferase activity exact : GlcN6P synthase activity exact : glucosamine 6-phosphate synthase activity exact : glucosamine--fructose-6-phosphate aminotransferase (isomerizing) activity exact : glucosamine-6-phosphate isomerase (glutamine-forming) activity exact : glucosamine-6-phosphate synthase activity exact : hexosephosphate aminotransferase activity exact : L-glutamine-D-fructose-6-phosphate amidotransferase activity exact : L-glutamine:D-fructose-6-phosphate isomerase (deaminating) broad : glucosaminephosphate isomerase
Cross-refs.	EC:2.6.1.16 MetaCyc:L-GLN-FRUCT-6-P-AMINOTRANS-RXN
Comment	none
Gene Product	1 polypeptide is linked to this Cvterm or one of its children.

Go to gene products section

TreeView

- GO:0003674 : molecular_function [6003 Gene Products]
  - GO:0003824 : catalytic activity [2894 Gene Products]
    - GO:0016740 : transferase activity [857 Gene Products]
      - GO:0016769 : transferase activity, transferring nitrogenous groups [17 Gene Products]
        - GO:0008483 : transaminase activity [13 Gene Products]
          - **GO:0004360 : glutamine-fructose-6-phosphate transaminase (isomerizing) activity [1 Gene Product]**

Gene Products

1 element (out of 1) is directly linked to the current term.

Identifier	Method	Evidence
ACYPI003246-PA	Blast2GO	IEA

user:
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HOME BROWSE PHYLOMES DOWNLOADS FAQ HELP ABOUT

ACYPI003246-PA | Search! | Blast Search! | Select phylomes

- ACYPI003246-PA
  - Info
  - Orthologs
  - Seed Trees (1)
    - Acyrthosiphon pisum phylome
  - Collateral Trees (1)
    - Tca0030316

Orthologs: ACYPI003246-PA (Download as a text table)

All orthology predictions [using 15 selected phylomes]

Species	orthologs
Drosophila pseudoobscura	Dps0001837_GA12297-PA
Drosophila_melanogaster	Dme0022158_FBpp0112410, Dme0032712_FBpp0084666
Tribolium castaneum	Tca0003720_Tca_GLEAN_02585
Pediculus humanus	Phu0009307_PHUM000728-PA
Drosophila yakuba	Dya0015071_FBpp0270402, Dya0001302_FBpp0255524
Homo_sapiens	Hsa0024925_ENSP00000253778, Hsa0017016_ENSP00000349860
Culex pipiens	Cpi0007757_CPIJ006769-PA, Cpi0007758_CPIJ006770-PA
Anopheles_gambiae	Aga0017741_AGAP011352-PA
Caenorhabditis_elegans	Cel0034026_F07A11.2a
Apis_mellifera	Ame0036256_GB18357-PA
Ciona_intestinalis	Cin0012315_ENSCINP00000003142
Drosophila mojavensis	Dmo0014089_FBpp0173590, Dmo0012506_FBpp0171988
Bombyx Mori	Bom0022140_BGIBMGA007517-PA
Nasonia vitripennis	Nvi0007906_hmm622374
Aedes aegypti	Aae0006955_AAEL009510-PA
Daphnia pulex	Dpu0020122_NCBI_GNO_152714

Orthologs prediction using phylome: Acyrthosiphon pisum phylome

Species	inparalogs	orthologs
Aedes aegypti	Api0003317_ACYPI003246-PA	Aae0006955_AAEL009510-PA
Culex pipiens	Api0003317_ACYPI003246-PA	Cpi0007757_CPIJ006769-PA, Cpi0007758_CPIJ006770-PA
Daphnia pulex	Api0003317_ACYPI003246-PA	Dpu0020122_NCBI_GNO_152714
Homo_sapiens	Api0003317_ACYPI003246-PA	Hsa0024925_ENSP00000253778, Hsa0017016_ENSP00000349860
Drosophila pseudoobscura	Api0003317_ACYPI003246-PA	Dps0001837_GA12297-PA
Drosophila_melanogaster	Api0003317_ACYPI003246-PA	Dme0022158_FBpp0112410, Dme0032712_FBpp0084666

user:
pass
login

HOME BROWSE PHYLOMES DOWNLOADS FAQ HELP ABOUT

ACYPI003246-PA | Search! | Blast Search! | Select phylomes

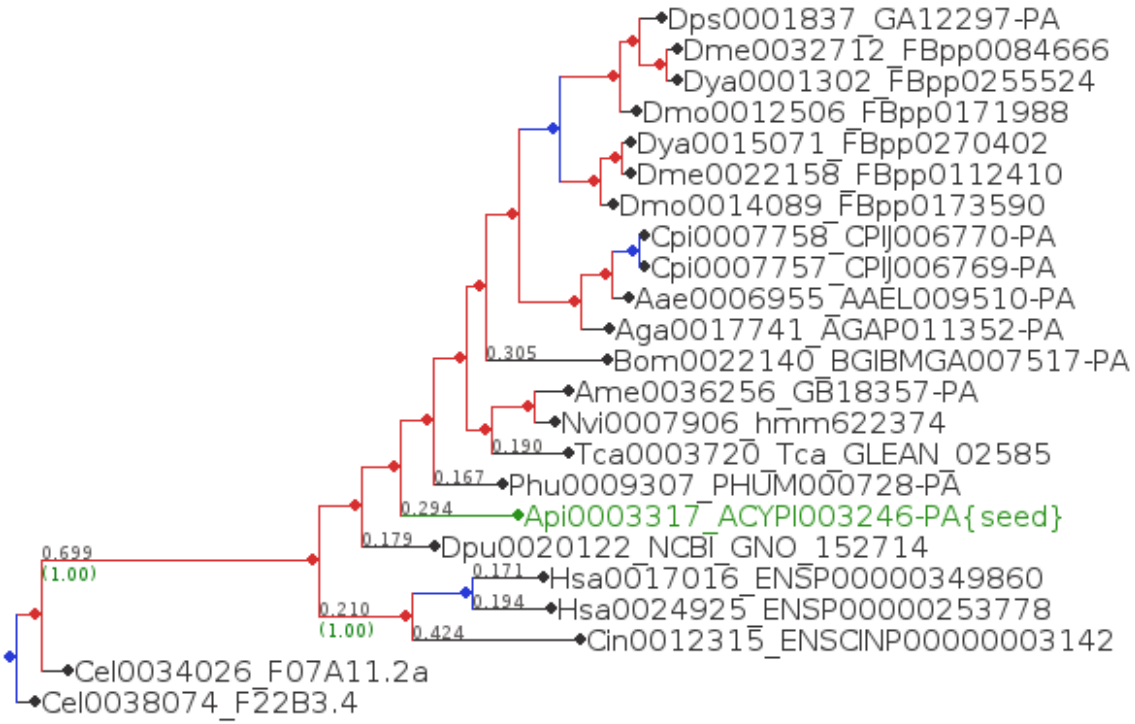
- ACYPI003246-PA
  - Info
  - Orthologs
  - Seed Trees (1)
    - Acyrthosiphon pisum phylome
  - Collateral Trees (1)
    - Tca0030316

Tree: Api0003317 (in phylome Acyrthosiphon pisum phylome)

Tree model: JTT (lk=-10685.600000) | – Download – | – Visualize (requires Java)–

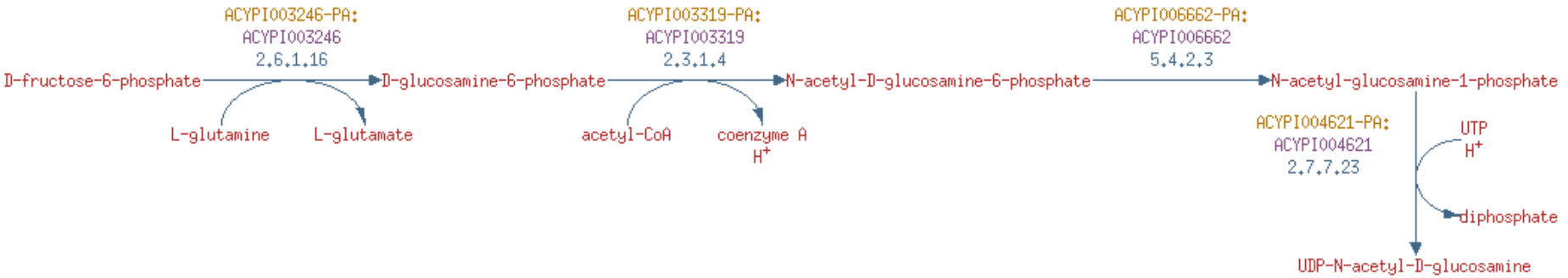
Tree Tools and Actions: Colapse tool | Search in tree | Clear

Branch scale: 0.101



Acyrthosiphon pisum (genome paper version) Pathway: UDP-*N*-acetyl-D-glucosamine biosynthesis II

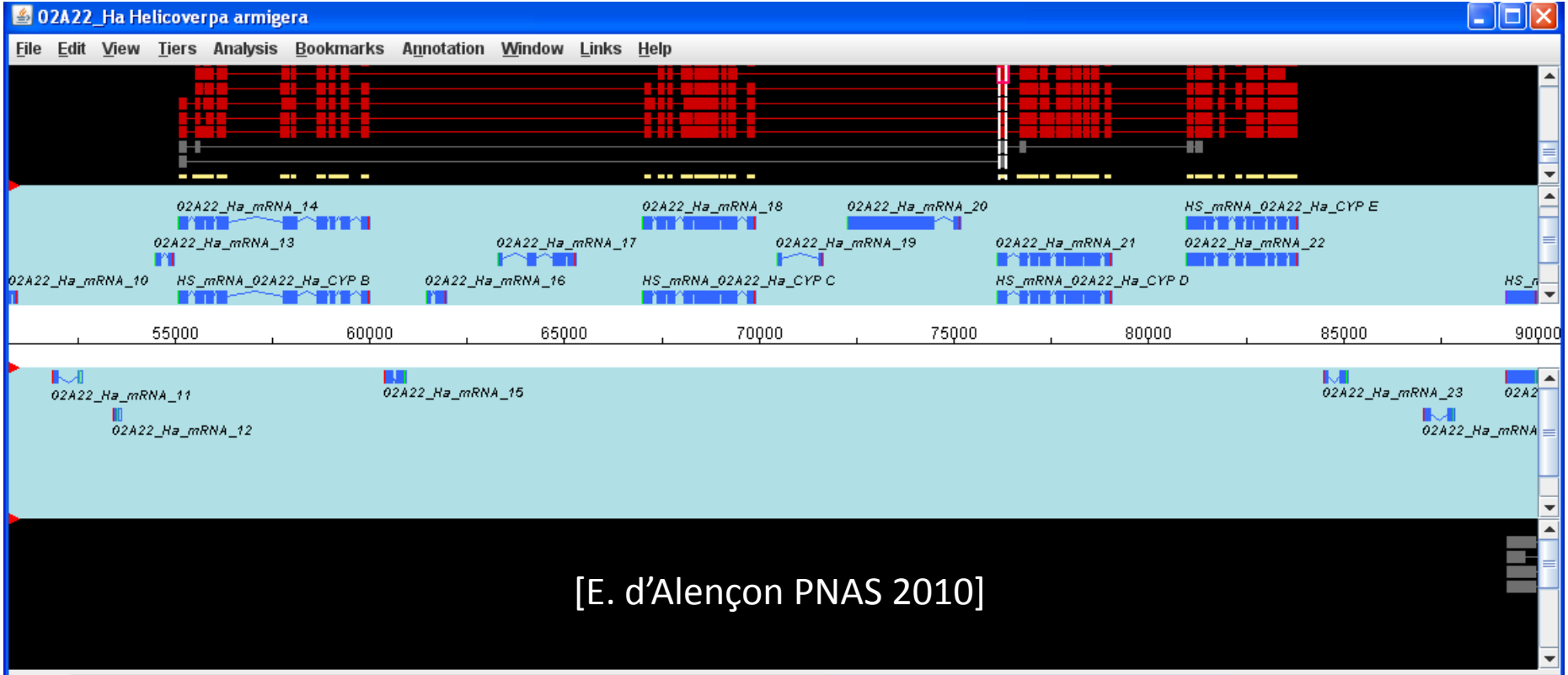
Show Predicted Enzymes | More Detail | Less Detail | Species Comparison



If an enzyme name is shown in bold, there is experimental evidence for this enzymatic activity.

Synonyms: UDP-*N*-acetylgalactosamine biosynthesis

Superclasses: Biosynthesis -> Amines and Polyamines Biosynthesis -> UDP-N-acetyl-D-glucosamine Biosynthesis



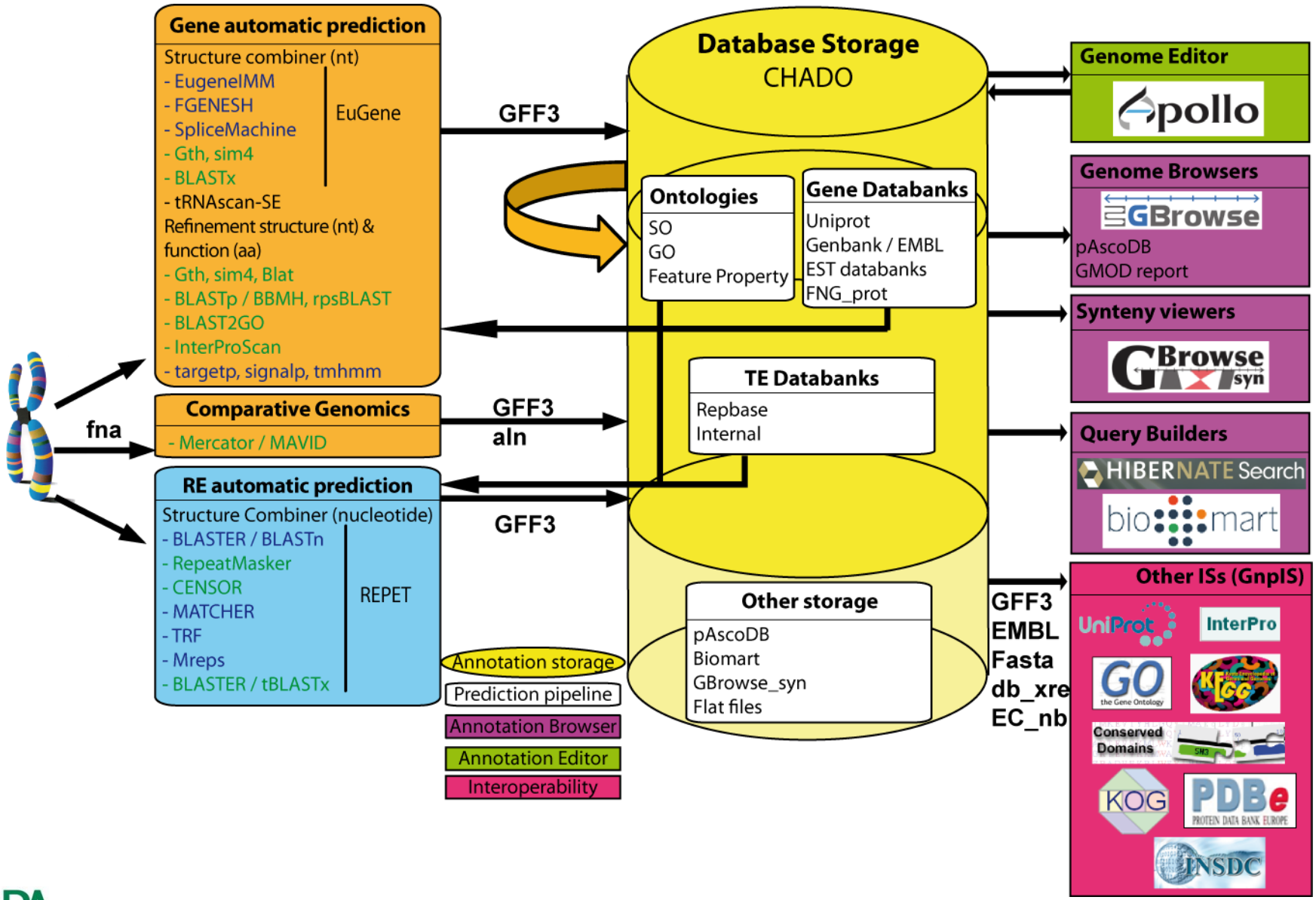
[E. d'Alençon PNAS 2010]

Type	Name	Range	Score
Helico-Spodo blastx S...	10N12_Sf_prot_06	55526-83473	0.0

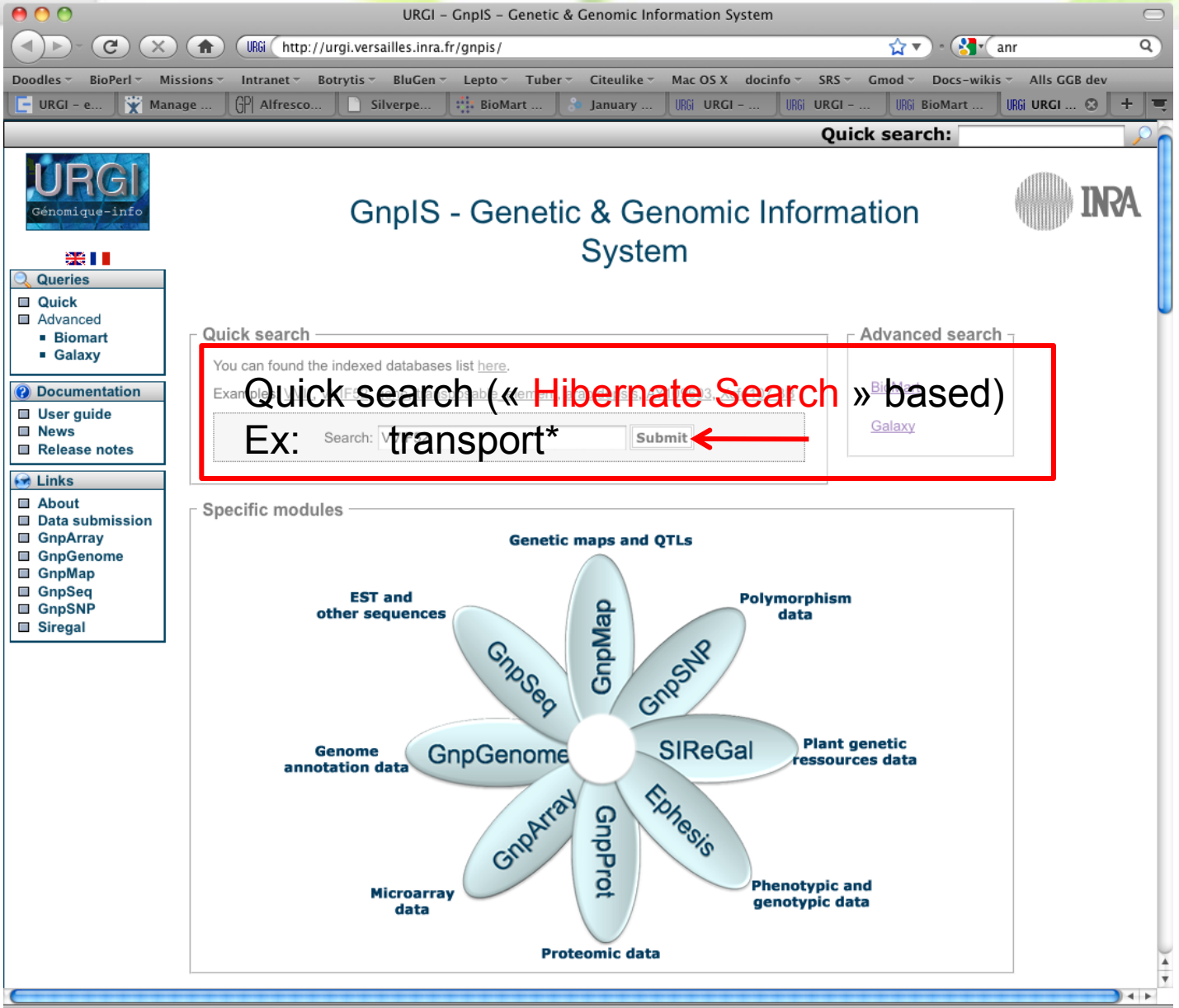
Helico-Spodo blastx Synteny: 10N12_Sf_prot_06

Genomic Range	Genomic Length	Genomic Length	Match Length	Genomic Range	Match Range	Score
55526-55705	180	180	61	55526-55705	64-124	0.0
55526-55705	180	180	61	55526-55705	64-124	0.0
55720-55965	246	246	84	55720-55965	95-178	0.0
55720-55965	246	246	84	55720-55965	95-178	0.0
56091-56315	225	225	76	56091-56315	168-243	0.0
56091-56315	225	225	76	56091-56315	168-243	0.0
57729-57926	198	198	67	57729-57926	216-282	0.0
57729-57926	198	198	67	57729-57926	216-282	0.0
58001-58096	96	96	33	58001-58096	280-312	0.0
58001-58096	96	96	33	58001-58096	280-312	0.0
58635-58853	219	219	74	58635-58853	313-386	0.0
58635-58853	219	219	74	58635-58853	313-386	0.0
58952-59080	129	129	44	58952-59080	378-421	0.0
58952-59080	129	129	44	58952-59080	378-421	0.0
59264-59431	168	168	57	59264-59431	420-476	0.0
59264-59431	168	168	57	59264-59431	420-476	0.0
67423-67548	126	126	45	67423-67548	79-123	0.0
67668-67778	111	111	38	67668-67778	118-156	0.0

Fungal CAS


Gene automatic prediction
Structure combiner (nt)
- EugeneIMM
- FGENESH
- SpliceMachine
- Gth, sim4
- BLASTx
EuGene
- tRNAscan-SE
Refinement structure (nt) & function (aa)
- Gth, sim4, Blat
- BLASTp / BBMH, rpsBLAST
- BLAST2GO
- InterProScan
- targetp, signalp, tmhmm
Comparative Genomics
- Mercator / MAVID
RE automatic prediction
Structure Combiner (nucleotide)
- BLASTER / BLASTn
- RepeatMasker
- CENSOR
- MATCHER
- TRF
- Mreps
- BLASTER / tBLASTx
REPET
fna
GFF3
GFF3
aln
GFF3
Database Storage
CHADO
Ontologies
SO
GO
Feature Property
Gene Databanks
Uniprot
Genbank / EMBL
EST databanks
FNG_prot
TE Databanks
Repbase
Internal
Other storage
pAscoDB
Biomart
GBrowse_syn
Flat files
GFF3
EMBL
Fasta
db_xre
EC_nb
Genome Editor
Apollo
Genome Browsers
GBrowse
pAscoDB
GMOD report
Synteny viewers
GBrowse_syn
Query Builders
HIBERNATE Search
biomart
Other ISs (GnpIS)
UniProt
InterPro
GO
the Gene Ontology
KEGG
Conserved Domains
KOG
PDBe
PROTEIN DATA BANK EUROPE
INSDC
Annotation storage
Prediction pipeline
Annotation Browser
Annotation Editor
Interoperability

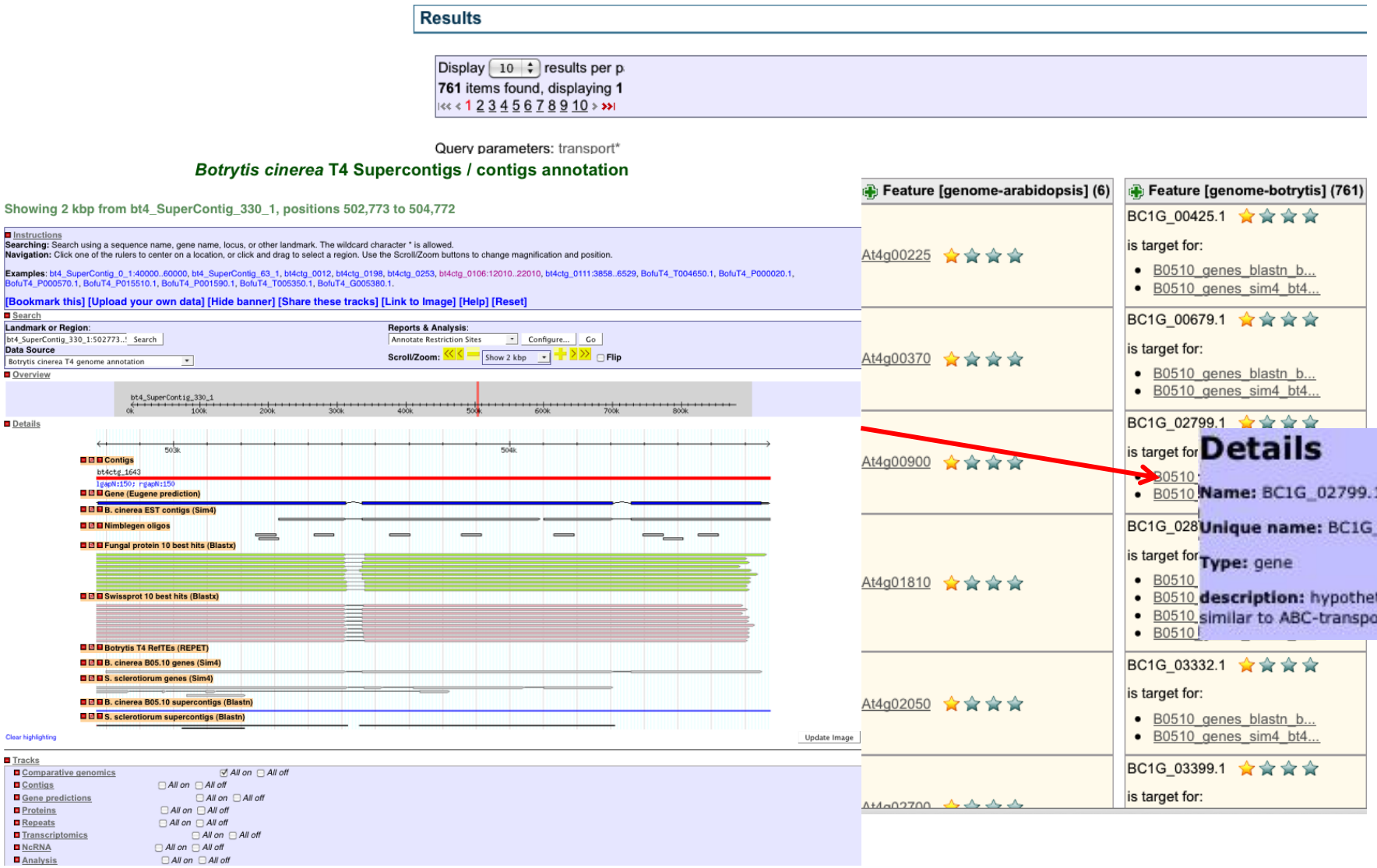
Quick and advanced search



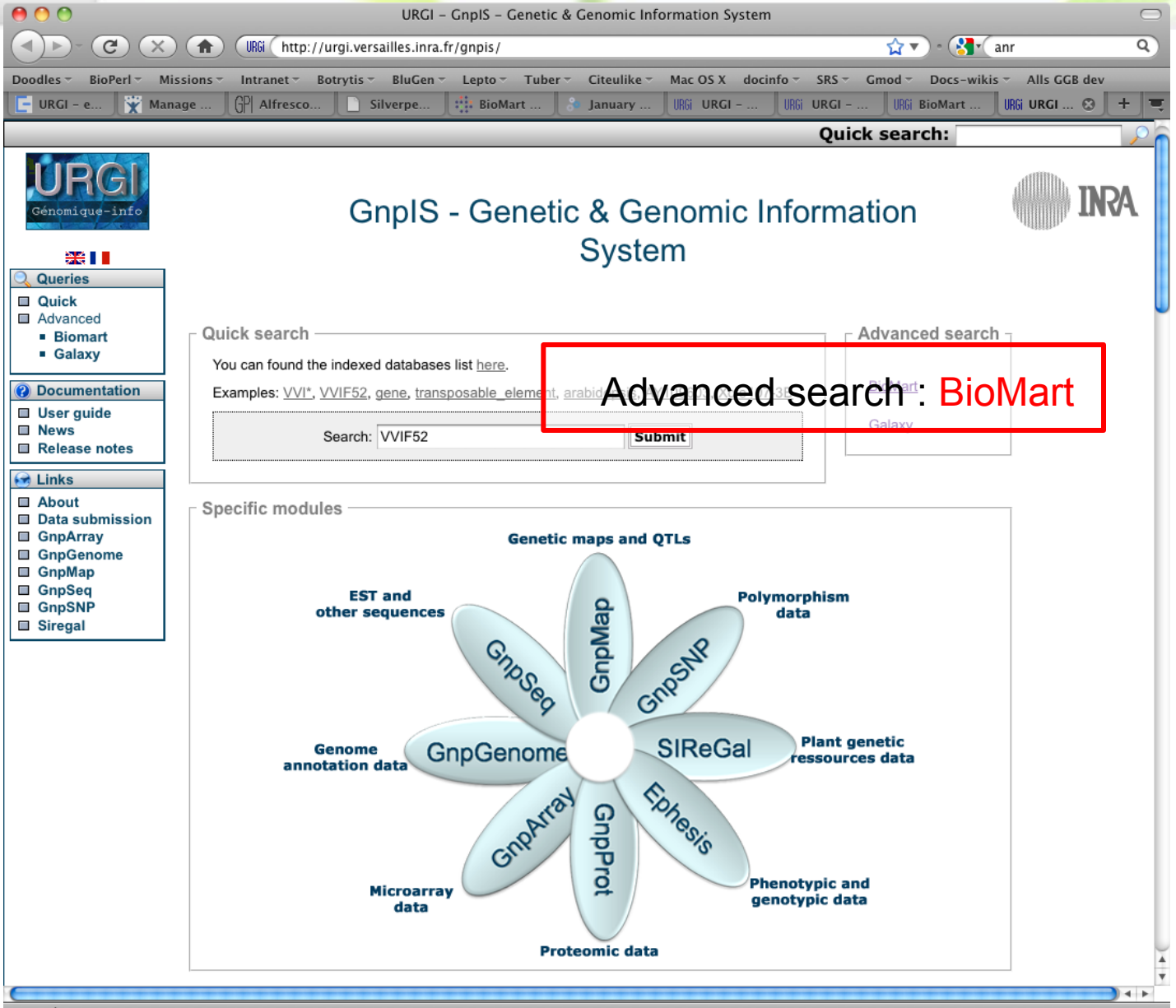
Quick search (« Hibernate Search » based)

Ex: transport*

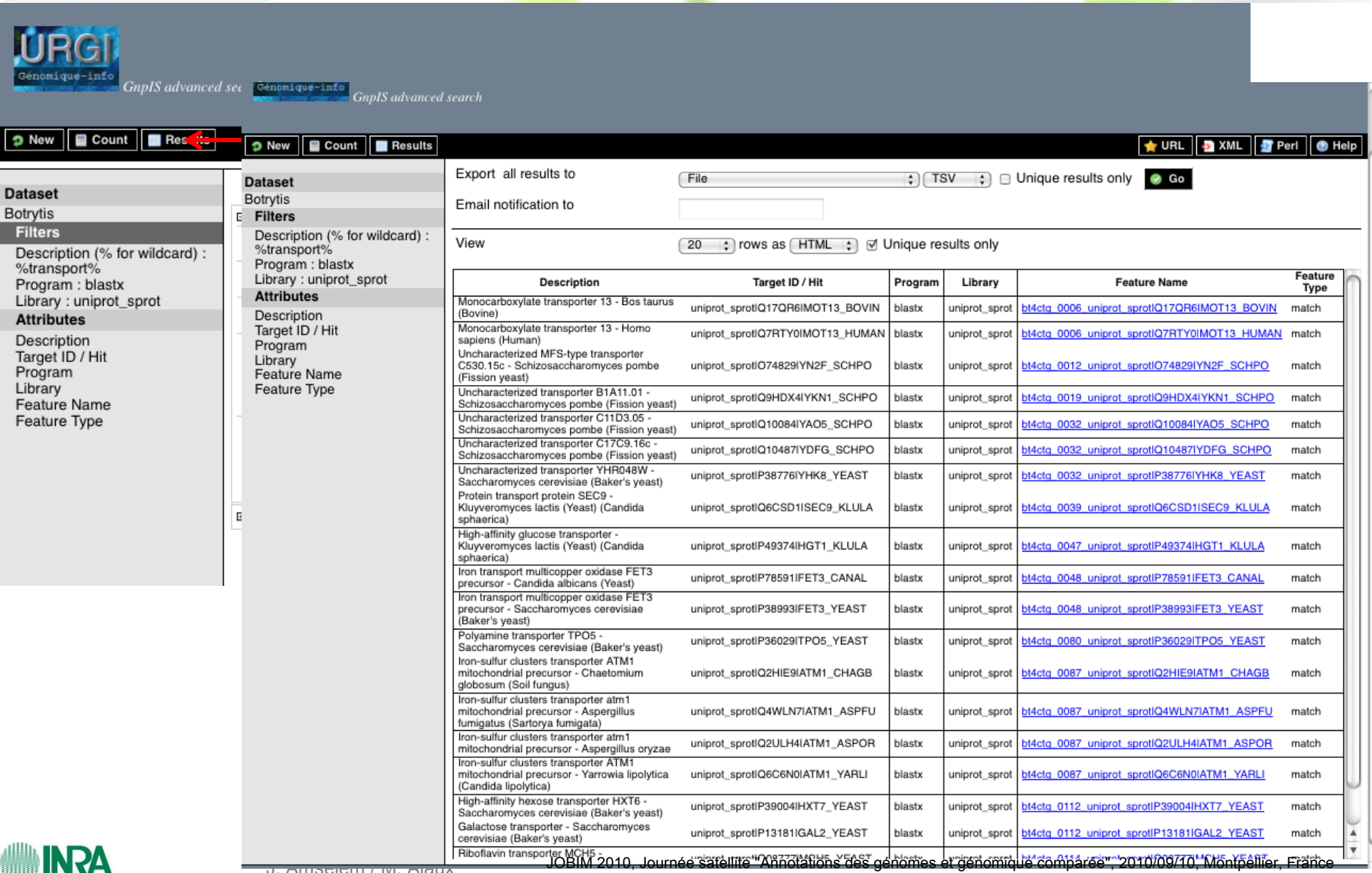
Quick search : Hibernate Search



Quick and advanced search



Advanced search : BioMart



Description	Target ID / Hit	Program	Library	Feature Name	Feature Type
Monocarboxylate transporter 13 - Bos taurus (Bovine)	uniprot_sprot|Q17QR6|MOT13_BOVIN	blastx	uniprot_sprot	bt4ctg_0006_uniprot_sprot|Q17QR6|MOT13_BOVIN	match
Monocarboxylate transporter 13 - Homo sapiens (Human)	uniprot_sprot|Q7RTY0|MOT13_HUMAN	blastx	uniprot_sprot	bt4ctg_0006_uniprot_sprot|Q7RTY0|MOT13_HUMAN	match
Uncharacterized MFS-type transporter C530.15c - Schizosaccharomyces pombe (Fission yeast)	uniprot_sprot|O74829|YN2F_SCHPO	blastx	uniprot_sprot	bt4ctg_0012_uniprot_sprot|O74829|YN2F_SCHPO	match
Uncharacterized transporter B1A11.01 - Schizosaccharomyces pombe (Fission yeast)	uniprot_sprot|Q9HDX4|YKN1_SCHPO	blastx	uniprot_sprot	bt4ctg_0019_uniprot_sprot|Q9HDX4|YKN1_SCHPO	match
Uncharacterized transporter C11D3.05 - Schizosaccharomyces pombe (Fission yeast)	uniprot_sprot|Q10084|YAO5_SCHPO	blastx	uniprot_sprot	bt4ctg_0032_uniprot_sprot|Q10084|YAO5_SCHPO	match
Uncharacterized transporter C17C9.16c - Schizosaccharomyces pombe (Fission yeast)	uniprot_sprot|Q10487|YDFG_SCHPO	blastx	uniprot_sprot	bt4ctg_0032_uniprot_sprot|Q10487|YDFG_SCHPO	match
Uncharacterized transporter YHR048W - Saccharomyces cerevisiae (Baker's yeast)	uniprot_sprot|P38776|YHK8_YEAST	blastx	uniprot_sprot	bt4ctg_0032_uniprot_sprot|P38776|YHK8_YEAST	match
Protein transport protein SEC9 - Kluyveromyces lactis (Yeast) (Candida sphaerica)	uniprot_sprot|Q6CSD1|SEC9_KLULA	blastx	uniprot_sprot	bt4ctg_0039_uniprot_sprot|Q6CSD1|SEC9_KLULA	match
High-affinity glucose transporter - Kluyveromyces lactis (Yeast) (Candida sphaerica)	uniprot_sprot|P49374|HGT1_KLULA	blastx	uniprot_sprot	bt4ctg_0047_uniprot_sprot|P49374|HGT1_KLULA	match
Iron transport multicopper oxidase FET3 precursor - Candida albicans (Yeast)	uniprot_sprot|P78591|FET3_CANAL	blastx	uniprot_sprot	bt4ctg_0048_uniprot_sprot|P78591|FET3_CANAL	match
Iron transport multicopper oxidase FET3 precursor - Saccharomyces cerevisiae (Baker's yeast)	uniprot_sprot|P38993|FET3_YEAST	blastx	uniprot_sprot	bt4ctg_0048_uniprot_sprot|P38993|FET3_YEAST	match
Polyamine transporter TPO5 - Saccharomyces cerevisiae (Baker's yeast)	uniprot_sprot|P36029|TPO5_YEAST	blastx	uniprot_sprot	bt4ctg_0080_uniprot_sprot|P36029|TPO5_YEAST	match
Iron-sulfur clusters transporter ATM1 mitochondrial precursor - Chaetomium globosum (Soil fungus)	uniprot_sprot|Q2HIE9|ATM1_CHAGB	blastx	uniprot_sprot	bt4ctg_0087_uniprot_sprot|Q2HIE9|ATM1_CHAGB	match
Iron-sulfur clusters transporter atm1 mitochondrial precursor - Aspergillus fumigatus (Sartorya fumigata)	uniprot_sprot|Q4WLN7|ATM1_ASPFU	blastx	uniprot_sprot	bt4ctg_0087_uniprot_sprot|Q4WLN7|ATM1_ASPFU	match
Iron-sulfur clusters transporter atm1 mitochondrial precursor - Aspergillus oryzae	uniprot_sprot|Q2ULH4|ATM1_ASPOR	blastx	uniprot_sprot	bt4ctg_0087_uniprot_sprot|Q2ULH4|ATM1_ASPOR	match
Iron-sulfur clusters transporter ATM1 mitochondrial precursor - Yarrowia lipolytica (Candida lipolytica)	uniprot_sprot|Q6C6N0|ATM1_YARLI	blastx	uniprot_sprot	bt4ctg_0087_uniprot_sprot|Q6C6N0|ATM1_YARLI	match
High-affinity hexose transporter HXT6 - Saccharomyces cerevisiae (Baker's yeast)	uniprot_sprot|P39004|HXT7_YEAST	blastx	uniprot_sprot	bt4ctg_0112_uniprot_sprot|P39004|HXT7_YEAST	match
Galactose transporter - Saccharomyces cerevisiae (Baker's yeast)	uniprot_sprot|P13181|GAL2_YEAST	blastx	uniprot_sprot	bt4ctg_0112_uniprot_sprot|P13181|GAL2_YEAST	match
Riboflavin transporter MCH5 -					

Homepage | GnpGenome | Blast | Downloads | Retrieve sequence

Leptosphaeria maculans

Functional annotation

Lema_P123290.1

+ Sequence
+ Domain/Motif (Interproscan results)
+ Localization / Targeting
+ Blast based analysis
+ Other analysis
+ Functionnal Gbrowse
+ Structural Gbrowse
+ Genome Mapping at gene locus

Synteny between Botrytis cinerea T4/B05.10 and Sclerotinia sclerotiorum

MERCATOR/MAVID based Clustering and alignments

Search

Landmark:
bt4_SuperContig_34_1:1..104 Search Reset

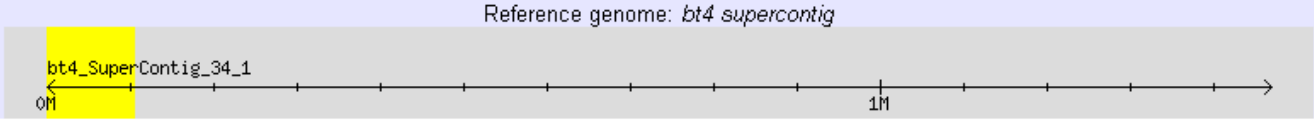
Genome to Search:
bt4 supercontig

Show 104.4 kbp

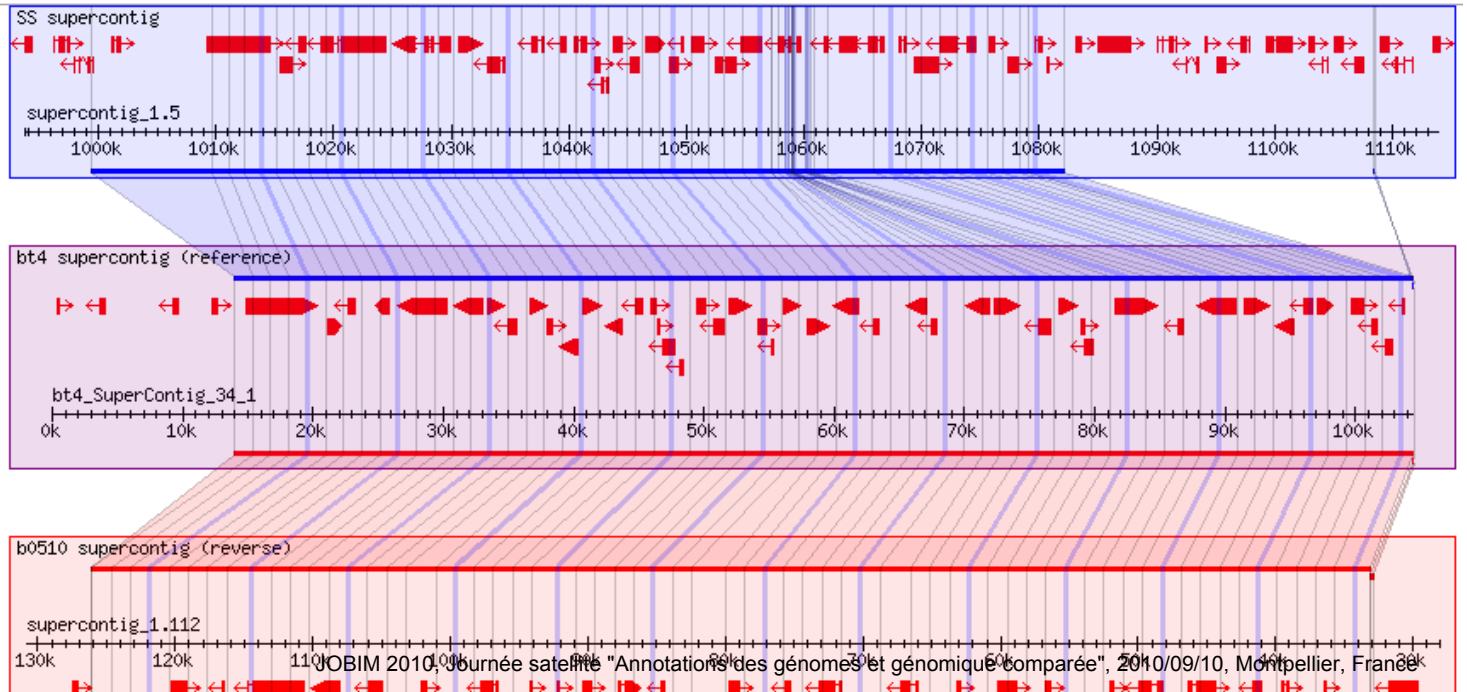
Aligned Species:
b0510 supercontig SS supercontig

Synteny between Botrytis cinerea T4/B05.10 and Sclerotinia sclerotiorum

Overview



SS_supercontig, b0510_supercontig



Conclusion

Place	Subject	Unit	Genomic size (Mb)	Gene nb			TE nb		
				predicted nb	curated nb	% curated	predicted nb	curated nb	% curated
Montpellier	Tropical plants	DAP CfL	23	5004	1982	39,61	3819	2703	70,78
Versailles	Fungi	BIOGER URGI	209	36325	2403	6,62	4402	0	0,00
Rennes	Insects	BIO3P BIVI SYMBIOSE	464	35907	1996	5,56	500501	800	0,16

Perspective

- Bioinformatics platform exchanges
  - Genome report editor
  - Annotation history integrated into GMOD report
- Publications
- Exploitation
  - Analyses of more species (*e.g.* cocoa, coffea, truffle)
  - Annotation of new features such as non-coding RNA, conserved non-coding sequence
  - Integration of new sequences such as those from new technologies
- CG
  - Compara
  - Tools for Evolutionary Biology Hackathon
- Web interfaces
  - GBrowse with Bio::DB::SeqFeature::Store::DBI::mysql
  - Jbrowse with chado postgresql
  - New Apollo
- Workflows
  - management (*e.g.* Galaxy, Jboss / jBPM, ETL)
  - Updates & reconcilers

Participants

Stéphanie Sidibe Bocs
Gaëtan Drocs
Valentin Guignon
Manuel Ruiz

Mathieu Rouard

Michaël Alaux
Baptiste Brault
Nathalie Choisne
Erik Kimmel
Isabelle Luyten
Delphine Steinbach
Hadi Quesneville

Philippe Leroy

GDEC

Spo

Nancy Terrier

Joelle Amselem
Adeline Simon
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Denis Tagu

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Fournier Philippe